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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/995,749A

DATE: 04/22/2002  
TIME: 17:19:02

Input Set : A:\Bo438cip.app  
Output Set: N:\CRF3\04222002\I995749A.raw

3 <110> APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA  
4 DIJKHUIZEN, LUBBERT  
5 RAHAOUI, HAKIM  
6 LEER, ROBERT-JAN

8 <120> TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES

10 <130> FILE REFERENCE: BO43388-CIP

12 <140> CURRENT APPLICATION NUMBER: 09/995,749A

13 <141> CURRENT FILING DATE: 2001-11-29

15 <150> PRIOR APPLICATION NUMBER: 09/604,957

16 <151> PRIOR FILING DATE: 2000-06-28

18 <150> PRIOR APPLICATION NUMBER: EPO 00201871.1

19 <151> PRIOR FILING DATE: 2000-05-25

21 <160> NUMBER OF SEQ ID NOS: 19

23 <170> SOFTWARE: PatentIn Ver. 2.1

25 <210> SEQ ID NO: 1

26 <211> LENGTH: 6026

27 <212> TYPE: DNA

28 <213> ORGANISM: Lactobacillus reuteri

30 <220> FEATURE:

31 <221> NAME/KEY: CDS

32 <222> LOCATION: (161)..(5503)

34 <400> SEQUENCE: 1

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39 cgataatcaa attgtttatt ttgatatgaa ggagattaaa atg gaa ata aag aaa 175  
40 Met Glu Ile Lys Lys  
41 1 5  
43 cat ttt aag ttg tac aaa agc ggc aaa caa tgg gta aca gca gca gtg 223  
44 His Phe Lys Leu Tyr Lys Ser Gly Lys Gln Trp Val Thr Ala Ala Val  
45 10 15 20  
47 gct acc gtt gcc gtt tca act gcg ctt ctt tac gga gga gtt gcg cat 271  
48 Ala Thr Val Ala Val Ser Thr Ala Leu Leu Tyr Gly Gly Val Ala His  
49 25 30 35  
51 gct gac caa caa gtt cag caa gct tcc acg act caa gac caa act tct 319  
52 Ala Asp Gln Gln Val Gln Gln Ala Ser Thr Thr Gln Asp Gln Thr Ser  
53 40 45 50  
55 acc gta aat aat gat act gat aaa aca gta gct tta gat act aat act 367  
56 Thr Val Asn Asn Asp Thr Asp Lys Thr Val Ala Leu Asp Thr Asn Thr  
57 55 60 65  
59 gac cag tca gct caa aca act gat aaa aaa caa gta gta tca aat act 415  
60 Asp Gln Ser Ala Gln Thr Thr Asp Lys Lys Gln Val Val Ser Asn Thr  
61 70 75 80  
63 aac caa agc aaa act gat gac act tca aca gct gat aag aat tct act 463

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68 Ser Thr Pro Val Ser Val Leu Pro Ser Asn Asn Thr Glu Lys Gln Ala
69          105          110          115
71 aaa aat tat aat gag caa gac aaa gga aac tat ggg aat att gat act 559
72 Lys Asn Tyr Asn Glu Gln Asp Lys Gly Asn Tyr Gly Asn Ile Asp Thr
73          120          125          130
75 gct tac ttt agc aat aat caa ttg cat gtt tca gga tgg aat gca acg 607
76 Ala Tyr Phe Ser Asn Asn Gln Leu His Val Ser Gly Trp Asn Ala Thr
77          135          140          145
79 aac gca tct caa gga aca aac agt cga caa atc att gtg cgt gat atc 655
80 Asn Ala Ser Gln Gly Thr Asn Ser Arg Gln Ile Ile Val Arg Asp Ile
81 150          155          160          165
83 aca acc aat aat gaa tta ggt cgc act gat gta aca aac aat gtt gca 703
84 Thr Thr Asn Asn Glu Leu Gly Arg Thr Asp Val Thr Asn Asn Val Ala
85          170          175          180
87 cgc cca gac gtt aag aat gtt cat aat gtt tat aac gct gat aat tct 751
88 Arg Pro Asp Val Lys Asn Val His Asn Val Tyr Asn Ala Asp Asn Ser
89          185          190          195
91 gga ttt gat gtt aat gtc aat att gac ttt agc aag atg aaa gat tat 799
92 Gly Phe Asp Val Asn Val Asn Ile Asp Phe Ser Lys Met Lys Asp Tyr
93          200          205          210
95 cgg gat tca att gaa att gtt agt cga tac agt gga aac ggt aaa tct 847
96 Arg Asp Ser Ile Glu Ile Val Ser Arg Tyr Ser Gly Asn Gly Lys Ser
97          215          220          225
99 gtt gac tgg tgg tcc caa ccg atc act ttt gac aaa aac aac tat gct 895
100 Val Asp Trp Trp Ser Gln Pro Ile Thr Phe Asp Lys Asn Asn Tyr Ala
101 230          235          240          245
103 tat ctt gat aca ttt gaa gtg aaa aat ggc gaa tta cat gca acc gga 943
104 Tyr Leu Asp Thr Phe Glu Val Lys Asn Gly Glu Leu His Ala Thr Gly
105          250          255          260
107 tgg aat gct act aat agt gcg att aac tat aat cac cat ttt gtg att 991
108 Trp Asn Ala Thr Asn Ser Ala Ile Asn Tyr Asn His His Phe Val Ile
109          265          270          275
111 ttg ttt gat caa acg aat ggt aaa gaa gta gca cga caa gaa gtt cgt 1039
112 Leu Phe Asp Gln Thr Asn Gly Lys Glu Val Ala Arg Gln Glu Val Arg
113          280          285          290
115 gaa ggt caa tca cgc cca gat gtt gct aag gta tat cca caa gta gtt 1087
116 Glu Gly Gln Ser Arg Pro Asp Val Ala Lys Val Tyr Pro Gln Val Val
117          295          300          305
119 ggt gct gcc aac tca ggc ttt aat gtg aca ttt aat atc agt gat tta 1135
120 Gly Ala Ala Asn Ser Gly Phe Asn Val Thr Phe Asn Ile Ser Asp Leu
121 310          315          320          325
123 gat tat act cac cag tac caa gtt ctt agt cgt tac agc aat tct gat 1183
124 Asp Tyr Thr His Gln Tyr Gln Val Leu Ser Arg Tyr Ser Asn Ser Asp
125          330          335          340
127 aat ggc gaa ggt gat aac gtt acc tac tgg ttt aat cca caa tcc att 1231
128 Asn Gly Glu Gly Asp Asn Val Thr Tyr Trp Phe Asn Pro Gln Ser Ile

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132 Ala Pro Ala Asn Gln Ser Asn Gln Gly Tyr Leu Asp Ser Phe Asp Ile				
133	360	365	370	
135 agt aaa aat ggt gaa gta aca gta act gga tgg aac gct act gac ttg				1327
136 Ser Lys Asn Gly Glu Val Thr Val Thr Gly Trp Asn Ala Thr Asp Leu				
137	375	380	385	
139 tca gaa tta caa aac aac cat tat gtg att cta ttt gat cag aca gca				1375
140 Ser Glu Leu Gln Asn Asn His Tyr Val Ile Leu Phe Asp Gln Thr Ala				
141 390	395	400	405	
143 ggc aaa caa gtt gca tct gct aaa gct gat tta att tca cgt cca gat				1423
144 Gly Lys Gln Val Ala Ser Ala Lys Ala Asp Leu Ile Ser Arg Pro Asp				
145	410	415	420	
147 gtt gct aaa gct tat cca aca gta aaa aca gct aca aat tct ggc ttc				1471
148 Val Ala Lys Ala Tyr Pro Thr Val Lys Thr Ala Thr Asn Ser Gly Phe				
149	425	430	435	
151 aag gta aca ttt aag gtt aat aac tta caa ccg ggt cac caa tac agc				1519
152 Lys Val Thr Phe Lys Val Asn Asn Leu Gln Pro Gly His Gln Tyr Ser				
153	440	445	450	
155 gtt gta agt cgt ttc tct gcc gat gaa aat ggt aat ggt aat gat aag				1567
156 Val Val Ser Arg Phe Ser Ala Asp Glu Asn Gly Asn Gly Asn Asp Lys				
157	455	460	465	
159 cgc cat aca gat tac tgg ttt agt cca gta ata tta aac cag act gct				1615
160 Arg His Thr Asp Tyr Trp Phe Ser Pro Val Ile Leu Asn Gln Thr Ala				
161 470	475	480	485	
163 tca aac att gat act att aca atg aca tct aat ggt tta cat att gca				1663
164 Ser Asn Ile Asp Thr Ile Thr Met Thr Ser Asn Gly Leu His Ile Ala				
165	490	495	500	
167 ggt tgg atg gca agt gat aac tca att aat gaa aca act cca tac gct				1711
168 Gly Trp Met Ala Ser Asp Asn Ser Ile Asn Glu Thr Thr Pro Tyr Ala				
169	505	510	515	
171 att atc ctc aat aat gga aaa gaa gtt act cgt caa aag atg agc tta				1759
172 Ile Ile Leu Asn Asn Gly Lys Glu Val Thr Arg Gln Lys Met Ser Leu				
173	520	525	530	
175 acc gcc cgt cca gat gta gca gca gta tat cct tca ctt tat aat agt				1807
176 Thr Ala Arg Pro Asp Val Ala Ala Val Tyr Pro Ser Leu Tyr Asn Ser				
177	535	540	545	
179 gct gtt agt ggt ttt gac act act att aaa ttg act aat gat caa tat				1855
180 Ala Val Ser Gly Phe Asp Thr Thr Ile Lys Leu Thr Asn Asp Gln Tyr				
181 550	555	560	565	
183 caa gcg ctt aat ggc caa tta caa gta ttg tta cgt ttt tct aaa gct				1903
184 Gln Ala Leu Asn Gly Gln Leu Gln Val Leu Leu Arg Phe Ser Lys Ala				
185	570	575	580	
187 gct gat ggt aat cca agt ggt gat aat act gta act gat caa ttt agt				1951
188 Ala Asp Gly Asn Pro Ser Gly Asp Asn Thr Val Thr Asp Gln Phe Ser				
189	585	590	595	
191 aaa aat tat gca act act ggt gga aac ttt gac tat gta aaa gta aat				1999
192 Lys Asn Tyr Ala Thr Thr Gly Gly Asn Phe Asp Tyr Val Lys Val Asn				
193	600	605	610	

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195 ggt aat caa gtt gaa ttt agt ggt tgg cac gca act aac caa tca aat 2047
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199 gat aaa gat tca caa tgg att att gtt tta gtt aat ggt aag gaa gta 2095
200 Asp Lys Asp Ser Gln Trp Ile Ile Val Leu Val Asn Gly Lys Glu Val
201 630                      635                      640                      645
203 aag cgt caa tta gtt aat gat act aaa gag gga gct gct ggc ttc aac 2143
204 Lys Arg Gln Leu Val Asn Asp Thr Lys Glu Gly Ala Ala Gly Phe Asn
205      650                      655                      660
207 cga aac gat gtc tac aaa gta aat cca gct att gaa aac agt tct atg 2191
208 Arg Asn Asp Val Tyr Lys Val Asn Pro Ala Ile Glu Asn Ser Ser Met
209      665                      670                      675
211 tct gga ttc caa ggc att att act tta cct gtg aca gtt aaa aac gaa 2239
212 Ser Gly Phe Gln Gly Ile Ile Thr Leu Pro Val Thr Val Lys Asn Glu
213      680                      685                      690
215 aat gtc caa ctt gtt cat cgg ttt agt aac gat gtg aag act ggt gaa 2287
216 Asn Val Gln Leu Val His Arg Phe Ser Asn Asp Val Lys Thr Gly Glu
217      695                      700                      705
219 ggt aac tat gtt gat ttc tgg tca gag cta atg cct gtt aag gat agc 2335
220 Gly Asn Tyr Val Asp Phe Trp Ser Glu Leu Met Pro Val Lys Asp Ser
221 710                      715                      720                      725
223 ttc caa aag ggg aat ggc cca ctt aag caa ttt ggc tta caa act att 2383
224 Phe Gln Lys Gly Asn Gly Pro Leu Lys Gln Phe Gly Leu Gln Thr Ile
225      730                      735                      740
227 aac ggt caa caa tat tat att gac cca aca act ggt caa cca cgt aag 2431
228 Asn Gly Gln Gln Tyr Tyr Ile Asp Pro Thr Thr Gly Gln Pro Arg Lys
229      745                      750                      755
231 aat ttc tta tta caa agt gga aat aat tgg att tac ttt gat agt gat 2479
232 Asn Phe Leu Leu Gln Ser Gly Asn Asn Trp Ile Tyr Phe Asp Ser Asp
233      760                      765                      770
235 act ggt gtg ggt act aat gca ctt gaa tta caa ttt gca aag gga act 2527
236 Thr Gly Val Gly Thr Asn Ala Leu Glu Leu Gln Phe Ala Lys Gly Thr
237      775                      780                      785
239 gtt tca tct aat gaa caa tac cgt aac ggt aat gca gct tac agt tat 2575
240 Val Ser Ser Asn Glu Gln Tyr Arg Asn Gly Asn Ala Ala Tyr Ser Tyr
241 790                      795                      800                      805
243 gat gac aag agt atc gaa aat gta aat ggt tac tta aca gca gat aca 2623
244 Asp Asp Lys Ser Ile Glu Asn Val Asn Gly Tyr Leu Thr Ala Asp Thr
245      810                      815                      820
247 tgg tac cgt cca aaa cag atc tta aag gat gga act acc tgg act gac 2671
248 Trp Tyr Arg Pro Lys Gln Ile Leu Lys Asp Gly Thr Thr Trp Thr Asp
249      825                      830                      835
251 tca aaa gaa aca gat atg cga cca atc ttg atg gta tgg tgg cct aat 2719
252 Ser Lys Glu Thr Asp Met Arg Pro Ile Leu Met Val Trp Trp Pro Asn
253      840                      845                      850
255 act ctt acc caa gca tac tac ctt aat tac atg aaa caa cat ggt aat 2767
256 Thr Leu Thr Gln Ala Tyr Tyr Leu Asn Tyr Met Lys Gln His Gly Asn
257      855                      860                      865
259 tta tta cca tct gct tta cca ttc ttt aat gcg gat gct gat cct gca 2815

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261 870 875 880 885
263 gaa tta aat cat tat tcc gaa att gtg caa caa aat att gaa aaa cga 2863
264 Glu Leu Asn His Tyr Ser Glu Ile Val Gln Gln Asn Ile Glu Lys Arg
265 890 895 900
267 att agt gaa acc gga aat act gat tgg tta cgt act tta atg cac gat 2911
268 Ile Ser Glu Thr Gly Asn Thr Asp Trp Leu Arg Thr Leu Met His Asp
269 905 910 915
271 ttt gtt act aac aat ccg atg tgg aat aag gat agt gaa aat gtt aac 2959
272 Phe Val Thr Asn Asn Pro Met Trp Asn Lys Asp Ser Glu Asn Val Asn
273 920 925 930
275 ttt agt ggt att caa ttc caa ggc gga ttc tta aag tat gaa aac tca 3007
276 Phe Ser Gly Ile Gln Phe Gln Gly Gly Phe Leu Lys Tyr Glu Asn Ser
277 935 940 945
279 gat tta acg cct tat gct aac tct gat tat cgc tta ctt ggt cgg atg 3055
280 Asp Leu Thr Pro Tyr Ala Asn Ser Asp Tyr Arg Leu Leu Gly Arg Met
281 950 955 960
283 cca atc aat att aag gat caa aca tat cgg gga caa gaa ttc cta ctt 3103
284 Pro Ile Asn Ile Lys Asp Gln Thr Tyr Arg Gly Gln Glu Phe Leu Leu
285 970 975 980
287 gct aac gat att gat aac tct aat cct gtt gtt caa gca gaa caa tta 3151
288 Ala Asn Asp Ile Asp Asn Ser Asn Pro Val Val Gln Ala Glu Gln Leu
289 985 990 995
291 aac tgg tta tac tat ctc ttg aac ttt gga acg atc aca gct aat aat 3199
292 Asn Trp Leu Tyr Tyr Leu Leu Asn Phe Gly Thr Ile Thr Ala Asn Asn
293 1000 1005 1010
295 gat caa gct aat ttt gat tct gta cgg gta gat gca ccg gat aat att 3247
296 Asp Gln Ala Asn Phe Asp Ser Val Arg Val Asp Ala Pro Asp Asn Ile
297 1015 1020 1025
299 gat gcc gat ctt atg aat atc gct cag gac tac ttt aat gct gca tat 3295
300 Asp Ala Asp Leu Met Asn Ile Ala Gln Asp Tyr Phe Asn Ala Ala Tyr
301 1030 1035 1040 1045
303 ggt atg gac tca gat gct gtc tca aat aag cat att aat att ctt gaa 3343
304 Gly Met Asp Ser Asp Ala Val Ser Asn Lys His Ile Asn Ile Leu Glu
305 1050 1055 1060
307 gac tgg aat cat gct gat ccg gaa tac ttt aat aag atc gga aat cca 3391
308 Asp Trp Asn His Ala Asp Pro Glu Tyr Phe Asn Lys Ile Gly Asn Pro
309 1065 1070 1075
311 caa ttg aca atg gat gat act att aag aat tcc ctg aat cat ggg ctt 3439
312 Gln Leu Thr Met Asp Asp Thr Ile Lys Asn Ser Leu Asn His Gly Leu
313 1080 1085 1090
315 tca gat gca act aat cgt tgg gga tta gat gca att gtt cat cag tca 3487
316 Ser Asp Ala Thr Asn Arg Trp Gly Leu Asp Ala Ile Val His Gln Ser
317 1095 1100 1105
319 tta gct gat cgt gaa aat aat tcc acg gaa aat gtt gta att cct aat 3535
320 Leu Ala Asp Arg Glu Asn Asn Ser Thr Glu Asn Val Val Ile Pro Asn
321 1110 1115 1120 1125
323 tac agt ttc gtt cgg gct cac gat aat aat tct caa gat caa att caa 3583
324 Tyr Ser Phe Val Arg Ala His Asp Asn Asn Ser Gln Asp Gln Ile Gln

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/995,749A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 9,15,18,21

Seq#:7; N Pos. 2,5,8,17,21

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:17; Line(s) 1454